

Fig. 1

10 20 30 40 50 60 70 80 90 100
 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

ClaI
 BspDI
 ATCGATAGTC GTCACCAAT GGATTTTCG ATTCTCTACT AGTCCATGGC TCACAATTTA CAAATCTCG AGAAAAGAAA GGATGCAAGG AGTATGAAGA 100

SpeI
 XhoI
 PaeR7I
 EarI

SspI
 DraI
 BstBI
 GGTTCCGAAT CTAATAATTT TAATTTAAAA AAATCAATTT CGAATTGAAA TTCAACTCCT ACTCGTTTTCG AAAATGCCAA TCCTTTAAGT AAATTTCTGG 200

BstBI
 ATCGCCCATTT TCTTCCAGAA ATTCTTTCAA AGTAGTGGTT TTGTACTGAT TTCTCCGCA AAGAATAGGA ACTTTCGAAT CTCTGGAGC GAAACGGGAT 300

SspI
 TTTSATAACA AAAAATATC CAGACAAACC ATAGGACTTT TTCAAATATT CCTATTTCG CTGTCCATTT GGAAGCAGCC AATCTTTAAC GCTGTCCAGC 400

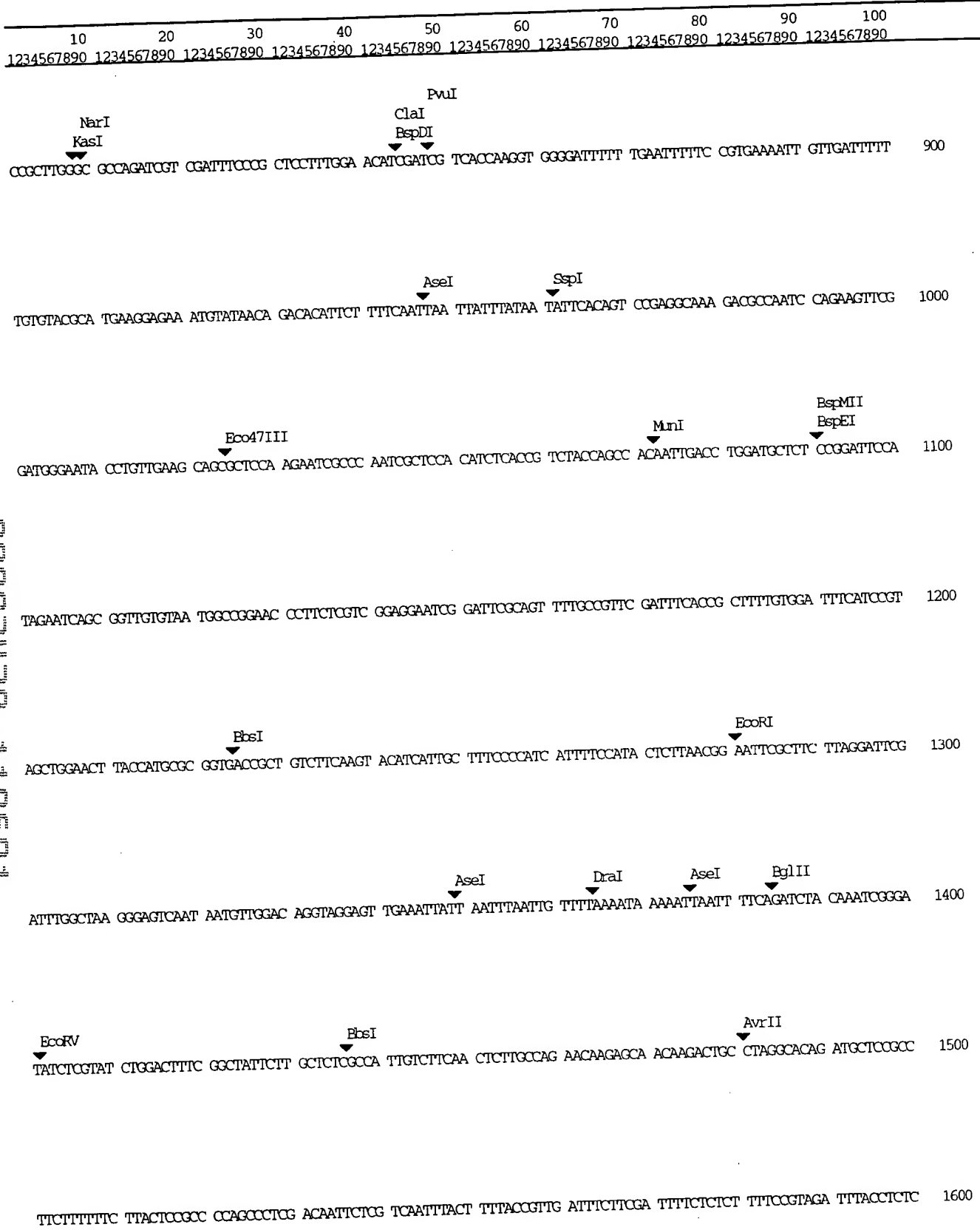
NcoI
 CAGAAGTGCT CCACTGCCA AGGATAAAG GCTCATTTTT GAAGCGAAT TTACTTAAAA TCTCTAGCCA TGGAGTCGAT GGATCAGAAA TTGAGGAAT 500

TTTAGATTTC ATCTTGAAAT TTGCAATGGA AAAAATAATT ATTCAAAGAA AATCACAGAA AATGCAACAA AAAAACAAA AAAAGAACA AAAACAAGTC 600

SmaI
 XbaI
 EarI
 Esp3I
 GAAAAGTGGC CCCGGTGGT TTGCTGAGC ATCTCTTCAA ACGAGACGG CTGCTGGCG ACTTCTCTG CCTGTGGGT GCATTTCCGC AACAAAATTC 700

AACACTTGTT TTGAAACGCA CCGCCCTGTT TCTTTTTC AATTTGATAA GAAAATCAGC ATTGTTTCAG GATGATTAC ATTCCAACTG CGATTTCTGTG 800

Fig. 2



F090T-024E660

Fig. 2

10 20 30 40 50 60 70 80 90 100
 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

EarI XbaI
 CTTCTGGTTT TTTTTCCTCT GCTAGAATG TATATTATGA TTATGAAAC GAATAAAAT TTTAGATGAC AGCTGCACG GCGACAACCT CGCTGACGAA 1700

TCGGCGGTAT CCGCGACGAA CGATGGCGAC TGGCGAGATG AAGGAGTTTC TGGGATAAA AGGCACAGAG CCCACGATT TTGGAATCAA TAGTGATGCT 1800

Mini EarI
 CAGGACTTGC CATCACCGAG TAGGCAGGCT TCGACGCGAA GAATGTCCAT CGGAGAGTCA ATTGATGGAA AAATCAATGA TTGGGAAGAG CCAAGGCTTG 1900

EcoRV SalI
 ATATCGAGGG ATTGTGGTA ATTTTAAAT TTTTGTGT AAATAAAAT TCTGCTGCT TCCAGGTGA CTATTTCAG CACCGAATCC GGCAAAACGG 2000

AATGGAATGG TTTGAGCAC CGGATTTGCC GTGTGGAGTG CAACCGAGC ACGAAATGAT GCGAGTTATG GGAACGATAT TCGAGAAGAA GCACGCGGAA 2100

BsaI PvuII
 AATTTTGAGA CTTCTGTGA GCAGCTGCTC GCAGTGCCCA GAATCTCATT TTCACGTAT CAGGATGTGG TTCGGACGGT TGGAAATGCA CAGACAGATC 2200

BstBI
 AATGTCCAAT GTCTTATGGA CGTTTGGTAA GGGAGAAAAT ACTGAAAAA AGTTTGCAA AATTGAAAA TTCGCCAGAA AGGTGGCAGA AAAACATTT 2300

GCAAAAATTG TTGTTTTCC TTCAGGAAAT CAGCAAACT TGGTCAAAA TAGCCCAATT ATGTGTCTTT TTTGAAAGTT TTCCATTAAA AAACACGAA 2400

D+DT

SspI D+DT D+T

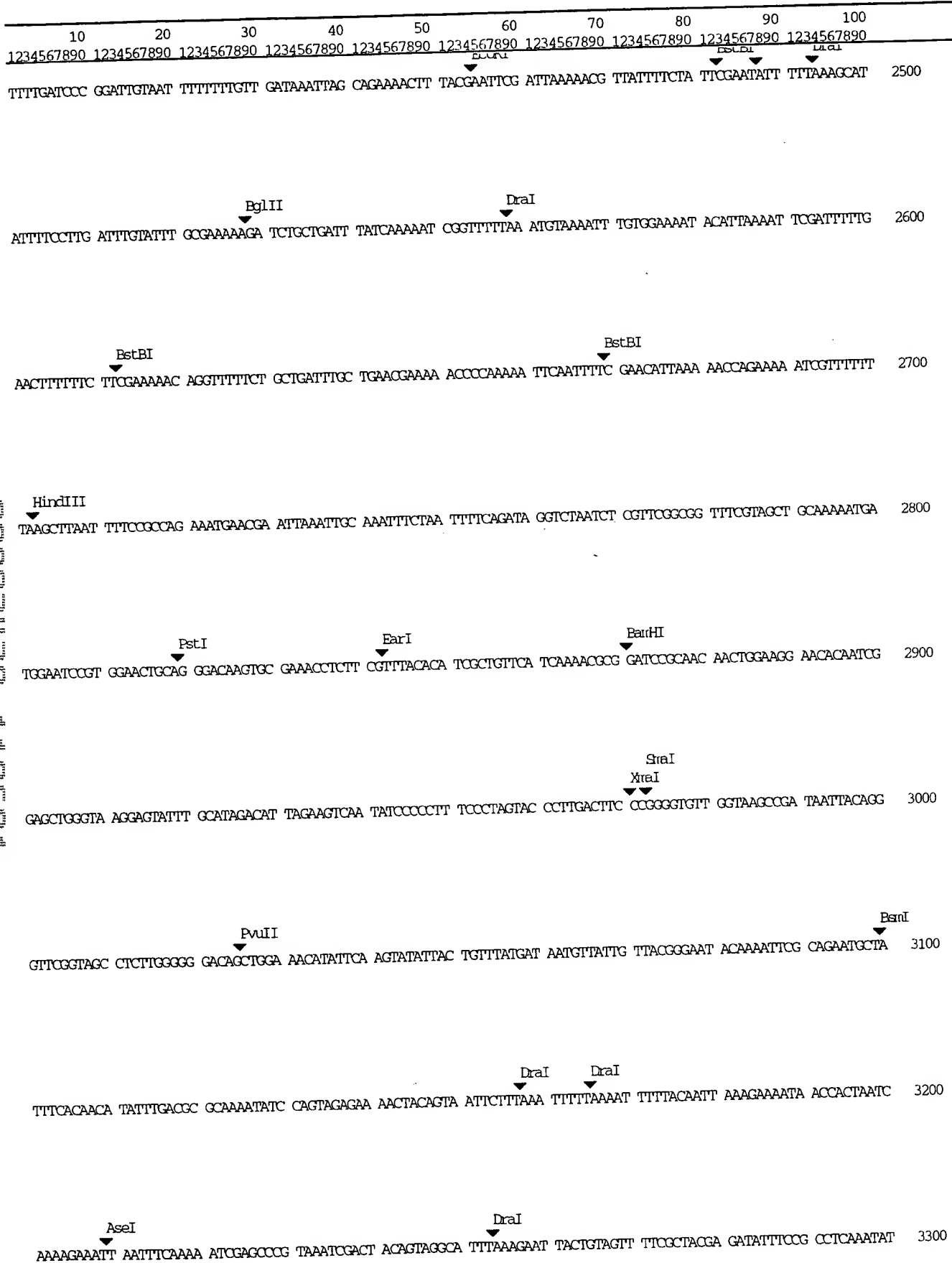


Fig. 2

10 20 30 40 50 60 70 80 90 100
 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

BsmI
 GTGTGCAAT ACGCATTAC GGATTTTGT GTTCCCGGA ATATGCTCTA AAGCATTATT TGTGAAATA AAAATCAAG AAAAAATTG CAGGACGACT 3400

BspHI
 TCATGACACT CGGAAAACAA ATGAAAGAGG ACTACGAACG AGCAGAAGCT GAAAAAGTGG GACGCCGAA GCAGAACAGA CGGTGGTGA TGATTGGCC 3500

PvuII AseI
 TGGAGTAACA GCTGGAGCCA TTGGAATCGT TGGAGTGTG GTGTGTGGC GGATGATGTT CAGCTTGAAG TAACGTATTC AATTGTGTGA AATAATTAA 3600

TTATGTACAA CTCCTTACAT TTGAATCTCA TTTTGTCTCA CTGATCTCT CATCCTTGA ACTGGAAGAA GTGGAAAGC TAGGCCACAA ATTACGGCTC 3700

MscI
 TCTGTGTGA TTTACGATTT TACTGCAATT TTTTCGATT GCTTTT TTTGGCAAAC CCTACTTCG CGTAATATCA ACTTTCCGT GTCTGTACA 3800

EarI
 TTTGTCAA AACCCTGAAA CCTAACTTT TCTGCGGTG GCTAGCCTC CGCTTCTCT TCCACATTC CAAAGTACC CTGTATCTCA ATAATTATC 3900

SplI BsiWI
 EarI MluI
 TTCATTAA CTGTCTTTT TGTGTGGC TCTTCCAAT CCCCCAAT TCCTGTACG GTACCGACT TTGTATTTAT TTTTTCAAA TTGTTTCTC 4000

TCTACAACAA CAAAAAAC GTTCTTTTA TTCAACCTT TTTTCGAAC GAACTGCAA TTTTGATAAT AGCGTGCGC AAGAGAATCC GGTTTTCATT 4100

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10 20 30 40 50 60 70 80 90 100
 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

XhoI

PaeR7I

Esp3I

EcoRI

TTGCCATCA CGTCATCCAA AAAAGITTAG TAGGAAAATA TCATTTTTTA ATATAATGAT TCATCTTTCT CGCTCTTCT GTCTCGAGAC GACGGTCAAT 4200

BstBI

TCGATGGCT TGAATTTTTC GAAACAAAA ATGTTTTTGT TTAGTGTAAG CGATCCCCC GCCTTATGCG TGTTTCACCA TCAGATAGGC TCGGCCATTT 4300

ApaLI

GATTCCTTG AATTTTGTG GTATATAAAA CAAAAACGT TAGTGACGA TTCAAAAAAC AACATGCGT GCTTTACTAT TCACCTCTGT TGTTCTTTTG 4400

EcoRI

EcoRI

GCTTTGGCTT TTGTTGAGGC AAAGAAGCAG ACTATCACTG TCAAGGTAC AACTATTTGT AATAAGAAGA GAATTCAGGM GRAGGITACC TTGGGAGAA 4500

StuI

AGATACCTGT GAGTTTTCAG TCTGTITTAG CTTGAAACGG CTTAAAAAG ACTAAAAAG CCTAAAAAT GAAGTTTTC ACCGTITTC AAAAGAAAGC 4600

CGAATTGCAC AGCTTTACAC GAGATTCTC AATAATTTGT ATTTGAAATT TTCATATCA TCCCAAACG TTCTTTACAC GAAATTTTC GATTTTGTG 4700

PsaI

DraI

CITAAAATAC GATACCTGT CTGACACGA AACATTTTG TTAATTTCAA AAAGATGTC GCCTTTAAAG AGTGCTGTAG TTGAAACTT CTGTGTGTC 4800

ClaI

BspDI

NruI

GGACTTTTCA TCGATTTTTC GTAGCGTTTT TTTATAAGAA AATGTATTT ATTTATTTCAA AAATTTAAT TTACCGAATC GCGAAAAACA AATGAAGAA 4900

SacI

MscI

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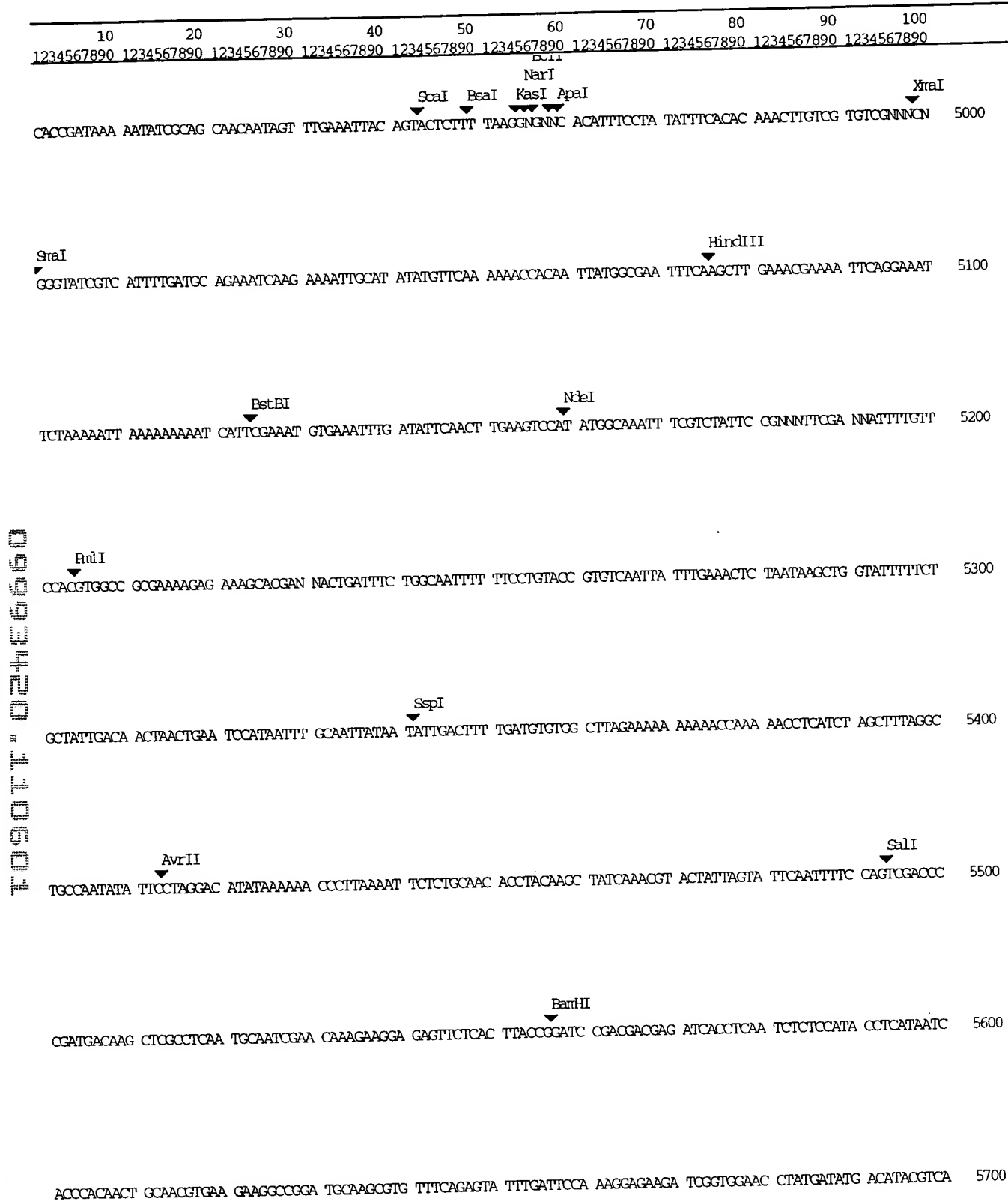
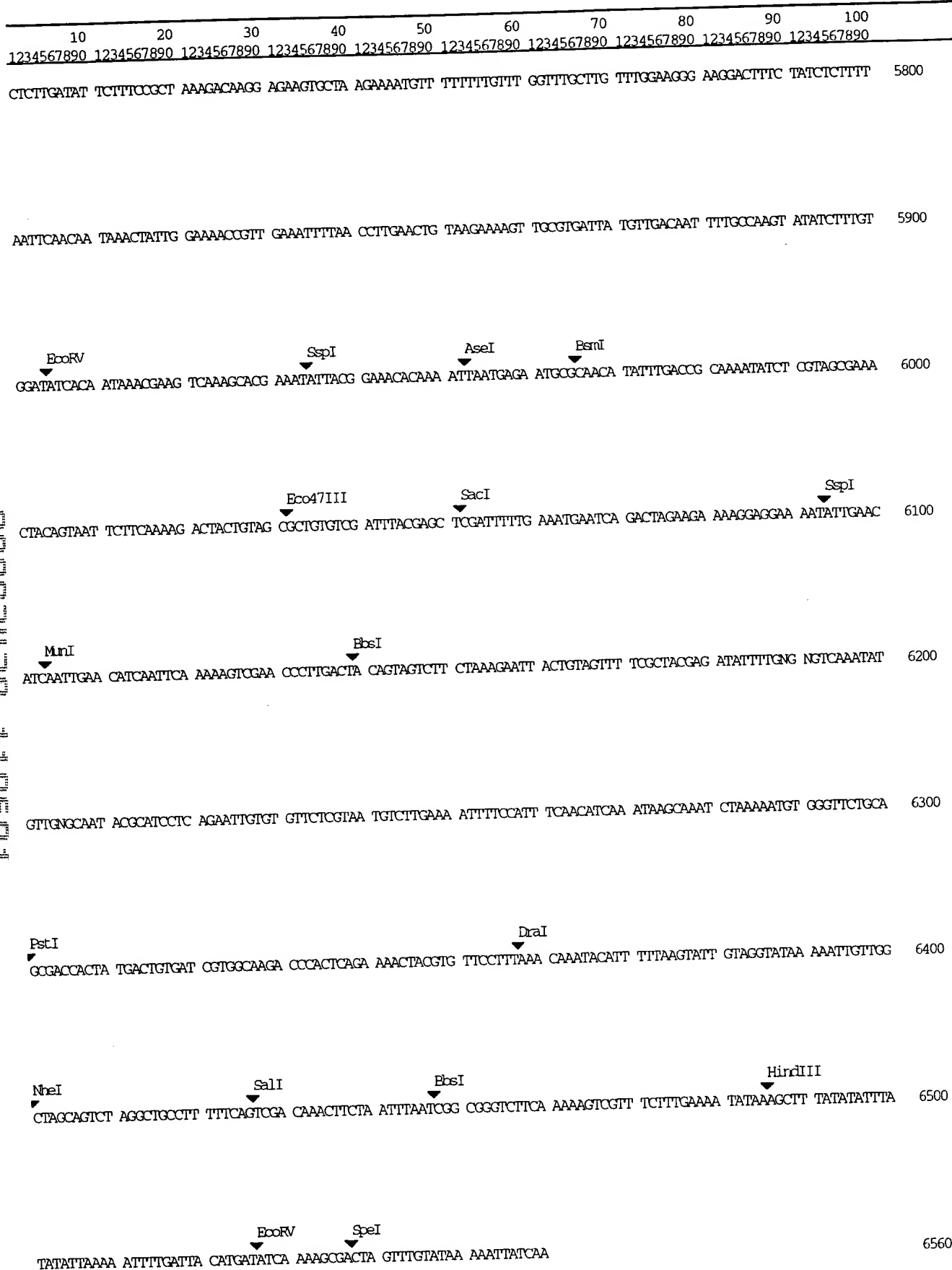


Fig. 2



T09011-024E6660

10 20 30 40 50 60 70 80 90 100
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

TTTGAGATGA CACGCTGCAC GGCGGACAAC TCGCTGACGA ATCCGGCGTA TCGGGCAGCA ACGATGGCGA CTGGCGAGAT GAAGGAGTTT CTGGGGATAA 100
MetT hrArgCysTh rAlaAspAsn SerLeuThrA snProAlaTy rArgArgArg ThrMetAlaT hrGlyGluMe tLysGluPhe LeuGlylleL

AAGGCACAGA GCCCACCAGT TTTGGAATCA ATAGTGATGC TCAGGACTTG CCATCACCGA GTAGGCAGGC TTCGACGCGA AGAATGTCCA TCGGAGAGTC 200
ysGlyThrGl uProThrAsp PheGlylleA snSerAspAl aGlnAspLeu ProSerProS erArgGlnAl aSerThrArg ArgMetSerI leGlyGluSe

EcoRV SalI
AATTGATGGA AAAATCAATG ATTGGGAAGA GCCAAGGCTT GATATCGAGG GATTGTGCTT CGACTATTTC ACGCACCAGT TCCGGCAAAA CGGAATGGAA 300
rileAspGly LysileAsnA spTrpGluGl uProArgLeu AspilleGluG lyPheValVa lAspTyrPhe ThrHisArgI leArgGlnAs nGlyMetGlu

TGTTTGGAG CACCGGGATT GCCCTGTGGA GTGCAACCGG AGCAGCAAAAT GATGCGAGTT ATGGGAACGA TATTCGAGAA GAAGCACGCG GAAAATTTTG 400
TrpPheGlyA laProGlyLe uProCysGly ValGlnProG luHisGluMe tMetArgVal MetGlyThrI lePheGluLy sLysHisAla GluAsnPheG

PvuII
AGACCTTCTG TGAGCAGCTG CTCGCAGTGC CCAGAATCTC ATTTTCACTG TATCAGGATG TGTTTCGGAC GGTGGAAAAT GCACAGACAG ATCAATGTCC 500
luThrPheCy sGluGlnLeu LeuAlaValP roArgileSe rPheSerLeu TyrGlnAspV alValArgTh rValGlyAsn AlaGlrThrA spGlnCysPr

PstI
AATGTCTTAT GGACGTTTGA TAGGTCTAAT CTCGTTCCGC GGTTCGCTAG CTGCAAAAAT GATGGAATCC GTGGAATGCG AGGGACAAGT GCGAAACCTC 600
oMetSerTyr GlyArgLeuI leGlyLeuII eSerPheGly GlyPheValA laAlaLysMe tMetGluSer ValGluLeuG lnGlyGlnVa lArgAsnLeu

BamHI BspHI
TTCGTTTACA CATCGCTGTT CATCAAAACG CGGATCCGCA ACAACTGGAA GGAACACAAT CGGAGCTGGG ACGACTTCAT GACACTCGGA AAACAAATGA 700
PheValTyrT hrSerLeuPh elleLysThr ArgilleArgA snAsnTrpLy sGluHisAsn ArgSerTrpA spAspPheMe tThrLeuGly LysGlnMetL

PvuII
AAGAGGACTA CGAACGAGCA GAAGCTGAAA AAGTGGGACG CCGGAAGCAG AACAGACGGT GGTGCGATGAT TGGCGCTGGA GTAACAGCTG GAGCCATTGG 800
ysGluAspTy rGluArgAla GluAlaGluL ysValGlyAr gArgLysGln AsnArgArgT rpSerMetIl eGlyAlaGly ValThrAlaG lyAlaIleGl

AseI
AATCGTTGGA GTCGCTGTGT GTGGGCGGAT GATGTTTACG TTGAAGTAAC GTATTCAATT TGTGTAAATA ATTAATTTAT GTACAACTCC TTACATTGGA 900
ylleValGly ValValValC ysGlyArgMe tMetPheSer LeuLys...

ATCTCATTTT KGCTCACTGA TTCTCTCATC CTTTGAAC TG GAAGAAGTGG GAAAGCTAGG CCACAAATTA CGGCTCTCTG TGTCGATTTA CGATTTTACT 1000

Bali
GCAATTTTTT CCGATTGCCT TTTTTTTTGG CCAAACCCTA CTTCGCGTA ATATCAACTT TTCCGTGTTC TGTACATTTC GTCAAAAACC CTGAAACCCT 1100

AACTTTTCTC GCCGTGGCCT AGCCTCCCGC TTCTCTTCCA CATTTCCAAA GTACCCCTGT ATCTCAATAA TTCATCTTCA CTTTAACTGT CTCTTTTCTG 1200

SplI MluI
GTGGCCTCTT CCAACTCCCC CCAATTCCT GTACGCGTAC GCGACTTTGT ATTTATTTTT TTCAAATTGT TTTCTCTCTA CAACAACAAA AAAACGGTT 1300

CAAAAAAAAA AAAAA

Fig. 3

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
MTRCTADNSL	TNPAYRRRTM	ATGEMKEFLG	IKGTEPTDFG	INSDAQDLPS	50
PSRQASTRM	SIGESIDGKI	NDWEEPRLDI	EGFVVDYFTH	RIRQNGMEWF	100
GAPGLPCGVQ	PEHEMMRVMG	TTFEKKHAEN	FETFCEQLLA	VPRISFSLYQ	150
DVVRTVGNAQ	TDQCPMSYGR	LIGLISFGGF	VAAKMMESVE	LQGQVRNLFV	200
YTSLFIKTRI	RNNWKEHNRS	WDDFMTLGKQ	MKEDYERAEA	EKVGRRKQNR	250
RWSMIGAGVT	AGAIGIVGVV	VCGRMMFSLK			280

Fig. 4

MTRCTADNSL TNPAYRRRTM ATGEMKEFLG IKGTEPTDFG INSDAQDLPS 50

PSRQASTRRM SIGESIDGKI NDWEEPRLDI EGFVVDYFTH RIRQNGMEWF 100

n1653ts (TAT -> AAT) N

GAPGLPCGVQ PEHEMMRVMG TIFEKKHAEN FETFCEQLLA VPRISFSLYQ 150

E (GGA -> GAA) n1950

DVVRTVGNAQ TDQCPMSYGR LIGLISFGGF VAAKMESVE LQGQVRNLFV 200

STOP (CAG -> TAG) n2077

YTSLFIKTRI RNNWKEHNRS WDDFMTLGKQ MKEDYERAEA EKVGRRKQNR 250

RWSMIGAGVT AGAIGIVGVV VCGRMMFSLK 280

Fig. 5

Quality:	89.8	Length:	298
Ratio:	0.376	Gaps:	11
Percent Similarity:	47.059	Percent Identity:	23.077

Fig. 6

1 GCGCCCGCCC CTCCGCGCCG CCTGCCCCGC CGCCCGCCGC GCTCCCGCCC
 51 GCCGCTCTCC GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA
 101 GGTGCCGGGG CTCCGGGCCC TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC
 151 GAACTGCGCG ACGGGAGGTC CGGGAGGCGA CCGTAGTCGC GCCGCCGCGC
 201 AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG GGGTGCGCCG
 251 GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC
 301 ATCCTTTTTTA GGAAAAGAGG GAAAAAATAA AACCCCTCCC CACCACCTCC
 351 TTCTCCCCAC CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG
 401 GCACCGGCGG GCCAGGCGCG TCCTGCCTTC ATTTATCCAG CAGCTTTTCG
 451 GAAAATGCAT TTGCTGTTTC GAGTTTAATC AGAAGACGAT TCCTGCCTCC

Fig. 7-1

10993420-110601

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501 GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT CCTGGGGAGG
551 CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT
601 GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCCA
651 ATACCGGACT GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAA
701 AACTCGAGCT CTTGAGATCT CCGGTTGGGA TTCCTGCGGA TTGACATTTC
751 TGTGAAGCAG AAGTCTGGGA ATCGATCTGG AAATCCTCCT AATTTTTACT
801 CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA TCAGCTATAA
851 CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG
901 GTTTTACAAA AAGGAACTT GACAGAGGAT CATGCTGTAC TTAAAAATA
951 CAAGTAAGTC TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC
1001 CTTTGAGATT TTTTACTTAA AGTGCATTCT AGTAAATTTA ATTTCCAGGC
1051 AGCTTAATAC ATTGTTTTTA GCCGTGTTAC TTGTAGTGTG TATGCCCTGC
1101 TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA CTTATTAGTT
1151 TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA
1201 CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA
1251 TTGGAATAAA AATTCCTGCT GTCTCATGCC AAGAGGGAAA CACCAGAATC
1301 AAGTGTTCCTG CGTGATTGAA GACACCCCTT CGTCCAAGAA TGCAAAGCAC
1351 ATCCAATAAA ATAGCTGGAT TATAACTCCT CTTCTTTCTC TGGGGGCCGT
1401 GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT GCTTTTCCTC
1451 TGGGAAGGAT GGCGCACGCT GGGAGAACGG GGTACGACAA CCGGGAGATA
1501 GTGATGAAGT ACATCCATTA TAAGCTGTCT CAGAGGGGCT ACGAGTGGGA
1551 TGCGGGAGAT GTGGGCGCCG CGCCCCCGGG GGCCGCCCCC GCACCGGGCA
1601 TCTTCTCCTC CCAGCCCGGG CACACGCCCC ATCCAGCCGC ATCCGCGAC
1651 CCGGTCGCCA GGACCTCGCC GCTGCAGACC CCGGCTGCCC CCGGCGCCGC
1701 CGCGGGGCCT GCGCTCAGCC CCGTGCCACC TGTGGTCCAC CTGGCCCTCC
1751 GCCAAGCCGG CGACGACTTC TCCCGCCGCT ACCGCGGCGA CTTGCGCGAG
1801 ATGTCCAGCC AGCTGCACCT GACGCCCTTC ACCGCGCGGG GACGCTTTGC
1851 CACGGTGGTG GAGGAGCTCT TCAGGGACGG GGTGAACTGG GGGAGGATTG
1901 TGGCCTTCTT TGAGTTCGGT GGGGTCATGT GTGTGGAGAG CGTCAACCGG

Fig. 7-2

0993420-110601

1951 GAGATGTCGC CCCTGGTGGA CAACATCGCC CTGTGGATGA CTGAGTACCT
2001 GAACCGGCAC CTGCACACCT GGATCCAGGA TAACGGAGGC TGGGATGCCT
2051 TTGTGGAACGT GTACGGCCCC AGCATGCGGC CTCTGTTTGA TTTCTCCTGG
2101 CTGTCTCTGA AGACTCTGCT CAGTTTGGCC CTGGTGGGAG CTTGCATCAC
2151 CCTGGGTGCC TATCTGAGCC ACAAGTGAAG TCAACATGCC TGCCCCAAAC
2201 AAATATGCAA AAGGTTCACT AAAGCAGTAG AAATAATATG CATTGTCAGT
2251 GATGTACCAT GAAACAAAGC TGCAGGCTGT TTAAGAAAAA ATAACACACA
2301 TATAAACATC ACACACACAG ACAGACACAC ACACACACAA CAATTAACAG
2351 TCTTCAGGCA AAACGTCGAA TCAGCTATTT ACTGCCAAAG GGAAATATCA
2401 TTTATTTTTT ACATTATTAA GAAAAAAGAT TTATTTATTT AAGACAGTCC
2451 CATCAAAACT CCGTCTTTGG AAATCCGACC ACTAATTGCC AAACACCGCT
2501 TCGTGTGGCT CCACCTGGAT GTTCTGTGCC TGTAAACATA GATTGCTTTT
2551 CCATGTTGTT GGCCGGATCA CCATCTGAAG AGCAGACGGA TGGAAAAAGG
2601 ACCTGATCAT TGGGGAAGCT GGCTTTCTGG CTGCTGGAGG CTGGGGAGAA
2651 GGTGTTTATT CACTTGCACT TCTTTGCCCT GGGGGCGTGA TATTAACAGA
2701 GGGAGGGTTC CCGTGGGGGG AAGTCCATGC CTCCCTGGCC TGAAGAAGAG
2751 ACTCTTTGCA TATGACTCAC ATGATGCATA CCTGGTGGGA GGAAAAGAGT
2801 TGGGAACTTC AGATGGACCT AGTACCCACT GAGATTTCCT CGCCGAAGGA
2851 CAGCGATGGG AAAAATGCCC TTAAATCATA GGAAAGTATT TTTTAAAGCT
2901 ACCAATTGTG CCGAGAAAAG CATTTTAGCA ATTTATACAA TATCATCCAG
2951 TACCTTAAAC CCTGATTGTG TATATTCATA TATTTTGGAT ACGCACCCCC
3001 CAACTCCCAA TACTGGCTCT GTCTGAGTAA GAAACAGAAT CCTCTGGAAC
3051 TTGAGGAAGT GAACATTTCT GTGACTTCCG ATCAGGAAGG CTAGAGTTAC
3101 CCAGAGCATC AGGCCGCCAC AAGTGCCTGC TTTTAGGAGA CCGAAGTCCG
3151 CAGAACCTAC CTGTGTCCCA GCTTGGAGGC CTGGTCCTGG AACTGAGCCG
3201 GGCCCTCACT GGCCCTCTCC AGGGATGATC AACAGGGTAG TGTGGTCTCC
3251 GAATGTCTGG AAGCTGATGG ATGGAGCTCA GAATTCCTCT GTCAAGAAAG
3301 AGCAGTAGAG GGGTGTGGCT GGGCCTGTCA CCCTGGGGCC CTCCAGGTAG
3351 GCCCCTTTTC ACGTGGAGCA TAGGAGCCAC GACCCTTCTT AAGACATGTA

Fig. 7-3

00993420.110601

3401 TCACTGTAGA GGAAGGAAC AGAGGCCCTG GGCCTTCCTA TCAGAAGGAC
3451 ATGGTGAAGG CTGGGAACGT GAGGAGAGGC AATGGCCACG GCCCATTTTG
3501 GCTGTAGCAC ATGGCACGTT GGCTGTGTGG CTTGGCCAC CTGTGAGTTT
3551 AAAGCAAGGC TTAAATGAC TTTGGAGAGG GTCACAAATC CTAAAAGAAG
3601 CATTGAAGTG AGGTGTCATG GATTAATTGA CCCCTGTCTA TGGAATTACA
3651 TGTA AACAT TATCTTGTC CTGTAGTTTG GTTTTATTTG AAAACCTGAC
3701 AAAAAAAAAAG TTCCAGGTGT GGAATATGGG GGTATCTGT ACATCCTGGG
3751 GCATTAAAAA AAAATCAATG GTGGGGAAC ATAAAGAAGT AACAAAAGAA
3801 GTGACATCTT CAGCAAATAA ACTAGGAAAT TTTTTTTTCT TCCAGTTTAG
3851 AATCAGCCTT GAAACATTGA TGGAATAACT CTGTGGCATT ATTGCATTAT
3901 ATACCATTTA TCTGTATTAA CTTTGAATG TACTCTGTTC AATGTTTAAT
3951 GCTGTGGTTG ATATTTGAA AGCTGCTTTA AAAAAATACA TGCATCTCAG
4001 CGTTTTTTTG TTTTAATTG TATTTAGTTA TGGCCTATAC ACTATTTGTG
4051 AGCAAAGGTG ATCGTTTTCT GTTTGAGATT TTTATCTCTT GATTCTTCAA
4101 AAGCATTCTG AGAAGGTGAG ATAAGCCCTG AGTCTCAGCT ACCTAAGAAA
4151 AACCTGGATG TCACTGGCCA CTGAGGAGCT TTGTTTCAAC CAAGTCATGT
4201 GCATTTCCAC GTCAACAGAA TTGTTTATTG TGACAGTTAT ATCTGTTGTC
4251 CCTTTGACCT TGTTTCTTGA AGGTTTCCTC GTCCCTGGGC AATTCCGCAT
4301 TTAATTCATG GTATTCAGGA TTACATGCAT GTTTGGTTAA ACCCATGAGA
4351 TTCATTCACT TAAAAATCCA GATGGCGAAT GACCAGCAGA TTCAAATCTA
4401 TGGTGGTTTG ACCTTTAGAG AGTTGCTTTA CGTGGCCTGT TTCAACACAG
4451 ACCCACCCAG AGCCCTCCTG CCCTCCTTCC GCGGGGGCTT TCTCATGGCT
4501 GTCCTTCAGG GTCTTCCTGA AATGCAGTGG TCGTTACGCT CCACCAAGAA
4551 AGCAGGAAAC CTGTGGTATG AAGCCAGACC TCCCCGGCGG GCCTCAGGGA
4601 ACAGAATGAT CAGACCTTTG AATGATTCTA ATTTTAAAGC AAAATATTAT
4651 TTTATGAAAG GTTTACATTG TCAAAGTGAT GAATATGGAA TATCCAATCC
4701 TGTGCTGCTA TCCTGCCAAA ATCATTTTAA TGGAGTCAGT TTGCAGTATG
4751 CTCCACGTGG TAAGATCCTC CAAGCTGCTT TAGAAGTAAC AATGAAGAAC
4801 GTGGACGTTT TTAATATAAA GCCTGTTTTG TCTTTTGTG TTGTTCAAAC

Fig. 7-4

4851 GGGATTCACA GAGTATTTGA AAAATGTATA TATATTAAGA GGTCACGGGG
4901 GCTAATTGCT AGCTGGCTGC CTTTGTCTGT GGGGTTTTGT TACCTGGTTT
4951 TAATAACAGT AAATGTGCCC AGCCTCTTGG CCCCAGAACT GTACAGTATT
5001 GTGGCTGCAC TTGCTCTAAG AGTAGTTGAT GTTGCATTTT CCTTATTGTT
5051 AAAACATGT TAGAAGCAAT GAATGTATAT AAAAGC

Fig. 7-5

099420 J0501
T090T" 024E6660

EMS

$egl-1(sd) \text{ } \sigma^{\text{♂}}$ x $ced-9(n1950 \text{ } dm) \text{ } \phi$

$\frac{ced-9(n1950 \text{ } dm)}{+}$; $\frac{egl-1(sd)}{+}$ Common:
able to lay eggs

$\frac{ced-9(n1950 \text{ } dm \text{ } *)}{+ \quad +}$; $\frac{egl-1(sd)}{+}$ Rare:
egg-laying defective

Fig. 8

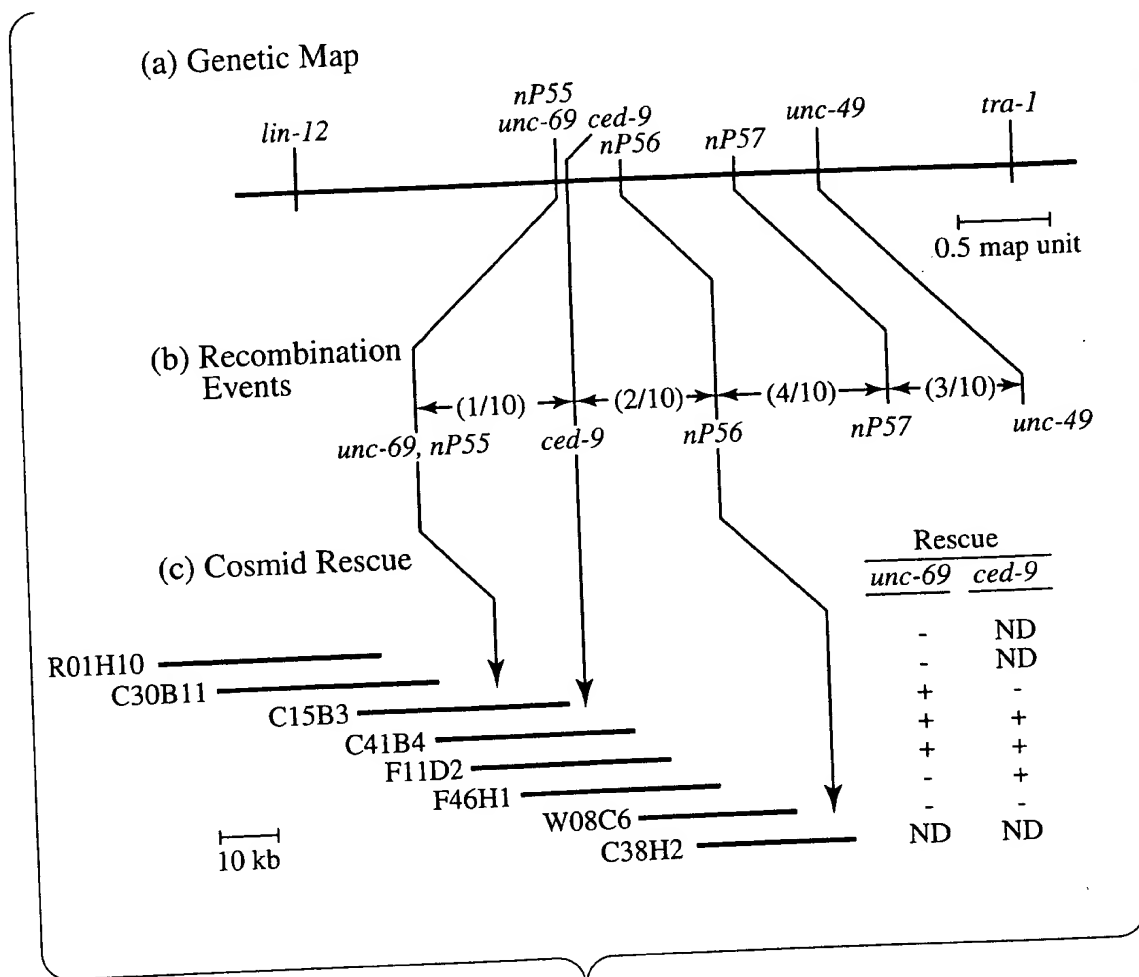


Fig. 9

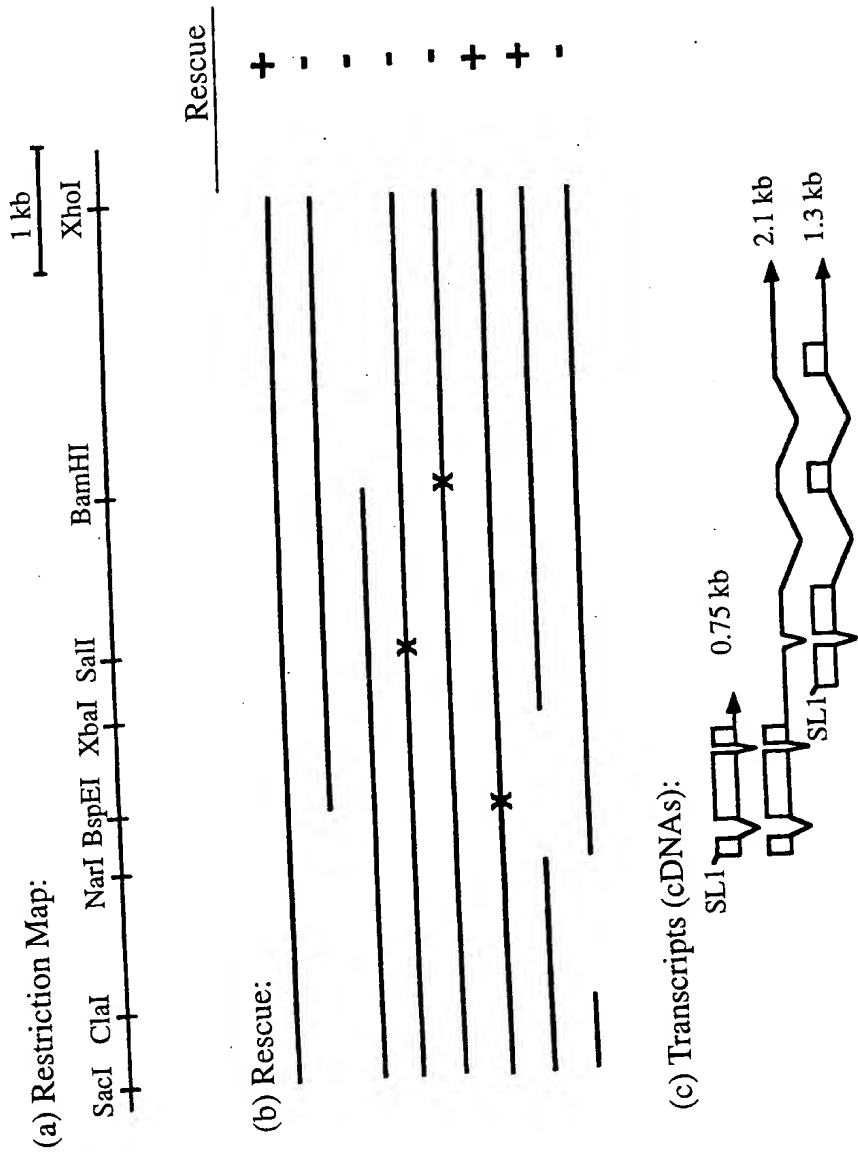


Fig. 10

Figure 11

n3400	
ATG ACA CGC TGC ACG GCG GAC AAC TCG CTG ACG AAT CCG CGG TAT CGG CGA CGA ACG ATG M T R C T A D N S L T N P A Y R R R T M	20
CCG ACT GGC GAG ATG AAG GAG TTT CTG GGG ATA AAA GGC ACA GAG CCC ACC GAT TTT GGA A T G E M K E F L G I K G T E P T D F G	40
ATC AAT AGT GAT GCT CAG GAC TTG CCA TCA CCG AGT AGG CAG GCT TCG ACG CGA AGA ATG I N S D A Q D L P S P S R Q A S T R R M	60
TCC ATC GGA GAG TCA ATT GAT GGA AAA ATC AAT GAT TGG GAA GAG CCA AGG CTT GAT ATC S I G E S I D G K I N D W E E P R L I	80
GAG GGA TTT GTG GTC GAC TAT TTC ACG CAC CGA ATC CGG CAA AAC GGA ATG GAA TGG TTT E G F V V D Y F T H R I R Q N G M E W F	100
BH4	
GGA GCA CCG GGA TTG CCG TGT GGA GTG CAA CCG GAG CAC GAA ATG ATG CGA GTT ATG GGA G A P G L P C G V Q P E H E M N R V M G	120
ACG ATA TTC GAG AAG AAG CAC GCG GAA AAT TTT GAG ACC TTC TGT GAG CAG CTG CTC GCA T I F E K K H A E N F E T F C E Q L L A	140
CTG CCC AGA ATC TCA TTT TCA CTG TAT CAG GAT GTG GTT CCG ACG GTT GCA AAT GCA CAG V P R I S F S L Y Q D V V R T V G N A Q	160
ACA GAT CAA TGT CCA ATG TCT TAT GGA CGT TTG ATA GGT CTA ATC TCG TTC GGC GGT TTC T D Q C P M S Y G R L I G L I S F G G F	180
BH1	
GTA GCT GCA AAA ATG ATG GAA TCC GTG GAA CTG CAG GGA CAA GTG CGA AAC CTC TTC GTT V A A K M M E S V E L Q G Q V R N L F V	200
TAC ACA TCG CTG TTC ATC AAA ACG CGG ATC CGC AAC AAC TGG AAG GAA CAC AAT CGG AGC Y T S L F I K T R I R N N W K E H N R S	220
BH2	
TGG GAC GAC TTC ATG ACA CTC GGA AAA ATG AAA GAG GAC TAC GAA CGA GCA GAA GCT W D D F M T L G K Q M K E D Y E R A E A	240
GAA AAA GTG GGA CGC CGG AAG CAG AAC AGA CCG TCG ATG ATT GGC GCT GGA GTA ACA E K V G R R K Q N R R W S M I G A G V T	260
GCT GGA GCC ATT GGA ATC GTT GGA GTC GTG TGT GGG CGG ATG ATG TTC AGC TTG AAG A G A I G I V G V V C G R M M F S L K	280